```
RAW SEQUENCE LISTING                  DATE: 01/28/2002
PATENT APPLICATION:  US/09/960,226    TIME: 13:49:07

       Input Set : A:\12243-19SeqLst.txt
       Output Set: N:\CRF3\01282002\I960226.raw
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 3 <110> APPLICANT: Rose, David
 4        Kuntz, Douglas
 5        Van Den Elsen, Jean
 7 <120> TITLE OF INVENTION: MANNOSIDASE STRUCTURES
 9 <130> FILE REFERENCE: 12243.19USU1
11 <140> CURRENT APPLICATION NUMBER: US 09/960,226
12 <141> CURRENT FILING DATE: 2001-09-21
14 <150> PRIOR APPLICATION NUMBER: US 60/263,458
15 <151> PRIOR FILING DATE: 2001-01-23
17 <150> PRIOR APPLICATION NUMBER: US 60/234,879
18 <151> PRIOR FILING DATE: 2000-09-22
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3198
26 <212> TYPE: DNA
27 <213> ORGANISM: Drosophila melanogaster
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(3198)
32 <223> OTHER INFORMATION:
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36 atg aag tta tgc ata tta ctg gcc gtc gtg gcc ttt gtt ggc ctc tcg      48
37 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala Phe Val Gly Leu Ser
38 1               5                  10                  15
40 ctc ggg aga tct agc cac cat cat cat cat cac gga gaa ttc gac gat      96
41 Leu Gly Arg Ser Ser His His His His His His Gly Glu Phe Asp Asp
42               20                  25                  30
44 cca ata aga cct cca ctt aaa gtg gct cgt tcc ccg agg cca ggg caa     144
45 Pro Ile Arg Pro Pro Leu Lys Val Ala Arg Ser Pro Arg Pro Gly Gln
46               35                  40                  45
48 tgc caa gat gtg gtc caa gac gtg ccc aat gtg gat gta cag atg ctg     192
49 Cys Gln Asp Val Val Gln Asp Val Pro Asn Val Asp Val Gln Met Leu
50        50                  55                  60
52 gag cta tac gat cgc atg tcc ttc aag gac ata gat gga ggc gtg tgg     240
53 Glu Leu Tyr Asp Arg Met Ser Phe Lys Asp Ile Asp Gly Gly Val Trp
54 65                  70                  75                  80
56 aaa cag ggc tgg aac att aag tac gat cca ctg aag tac aac gcc cat     288
57 Lys Gln Gly Trp Asn Ile Lys Tyr Asp Pro Leu Lys Tyr Asn Ala His
58               85                  90                  95
60 cac aaa cta aaa gtc ttc gtt gtg ccg cac tcg cac aac gat cct gga     336
61 His Lys Leu Lys Val Phe Val Val Pro His Ser His Asn Asp Pro Gly
62              100                 105                 110
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```
64  tgg att cag acg ttt gag gaa tac tac cag cac gac acc aag cac atc      384
65  Trp Ile Gln Thr Phe Glu Glu Tyr Tyr Gln His Asp Thr Lys His Ile
66          115                 120                 125
68  ctg tcc aat gca cta cgg cat ctg cac gac aat ccc gag atg aag ttc      432
69  Leu Ser Asn Ala Leu Arg His Leu His Asp Asn Pro Glu Met Lys Phe
70          130                 135                 140
72  atc tgg gcg gaa atc tcc tac ttt gct cgg ttc tat cac gat ttg gga      480
73  Ile Trp Ala Glu Ile Ser Tyr Phe Ala Arg Phe Tyr His Asp Leu Gly
74  145                 150                 155                 160
76  gag aac aaa aag ctg cag atg aag tcc att gta aag aat gga cag ttg      528
77  Glu Asn Lys Lys Leu Gln Met Lys Ser Ile Val Lys Asn Gly Gln Leu
78                  165                 170                 175
80  gaa ttg gaa ttt gtg act gga gga tgg gta atg ccg gac gag gcc aac      576
81  Glu Leu Glu Phe Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala Asn
82                  180                 185                 190
84  tcc cac tgg cga aac gta ctg ctg cag ctg acc gaa ggg caa aca tgg      624
85  Ser His Trp Arg Asn Val Leu Leu Gln Leu Thr Glu Gly Gln Thr Trp
86          195                 200                 205
88  ttg aag caa ttc atg aat gtc aca ccc act gct tcc tgg gcc atc gat      672
89  Leu Lys Gln Phe Met Asn Val Thr Pro Thr Ala Ser Trp Ala Ile Asp
90          210                 215                 220
92  ccc ttc gga cac agt ccc act atg ccg tac att ttg cag aag agt ggt      720
93  Pro Phe Gly His Ser Pro Thr Met Pro Tyr Ile Leu Gln Lys Ser Gly
94  225                 230                 235                 240
96  ttc aag aat atg ctt atc caa agg acg cac tat tcg gtt aag aag gaa      768
97  Phe Lys Asn Met Leu Ile Gln Arg Thr His Tyr Ser Val Lys Lys Glu
98                  245                 250                 255
100 ctg gcc caa cag cga cag ctt gag ttc ctg tgg cgc cag atc tgg gac      816
101 Leu Ala Gln Gln Arg Gln Leu Glu Phe Leu Trp Arg Gln Ile Trp Asp
102                 260                 265                 270
104 aac aaa ggg gac aca gct ctc ttc acc cac atg atg ccc ttc tac tcg      864
105 Asn Lys Gly Asp Thr Ala Leu Phe Thr His Met Met Pro Phe Tyr Ser
106         275                 280                 285
108 tac gac att cct cat acc tgt ggt cca gat ccc aag gtt tgc tgt cag      912
109 Tyr Asp Ile Pro His Thr Cys Gly Pro Asp Pro Lys Val Cys Cys Gln
110 290                 295                 300
112 ttc gat ttc aaa cga atg ggc tcc ttc ggt ttg agt tgt cca tgg aag      960
113 Phe Asp Phe Lys Arg Met Gly Ser Phe Gly Leu Ser Cys Pro Trp Lys
114 305                 310                 315                 320
116 gtg ccg ccg cgt aca atc agt gat caa aat gtg gca gca cgc tca gat     1008
117 Val Pro Pro Arg Thr Ile Ser Asp Gln Asn Val Ala Ala Arg Ser Asp
118                 325                 330                 335
120 ctg ctg gtt gat cag tgg aag aag aag gcc gag ctg tat cgc aca aac     1056
121 Leu Leu Val Asp Gln Trp Lys Lys Lys Ala Glu Leu Tyr Arg Thr Asn
122                 340                 345                 350
124 gtg ctg ctg att ccg ttg ggt gac gac ttc cgc ttc aag cag aac acc     1104
125 Val Leu Leu Ile Pro Leu Gly Asp Asp Phe Arg Phe Lys Gln Asn Thr
126         355                 360                 365
128 gag tgg gat gtg cag cgc gtg aac tac gaa agg ctg ttc gaa cac atc     1152
```

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129 Glu Trp Asp Val Gln Arg Val Asn Tyr Glu Arg Leu Phe Glu His Ile
130     370             375             380
132 aac agc cag gcc cac ttc aat gtc cag gcg cag ttc ggc aca ctg cag        1200
133 Asn Ser Gln Ala His Phe Asn Val Gln Ala Gln Phe Gly Thr Leu Gln
134 385             390             395             400
136 gaa tac ttt gat gca gtg cac cag gcg gaa agg gcg gga caa gcc gag        1248
137 Glu Tyr Phe Asp Ala Val His Gln Ala Glu Arg Ala Gly Gln Ala Glu
138             405             410             415
140 ttt ccc acg cta agc ggt gac ttt ttc aca tac gcc gat cga tcg gat        1296
141 Phe Pro Thr Leu Ser Gly Asp Phe Phe Thr Tyr Ala Asp Arg Ser Asp
142             420             425             430
144 aac tat tgg agt ggc tac tac aca tcc cgc ccg tat cat aag cgc atg        1344
145 Asn Tyr Trp Ser Gly Tyr Tyr Thr Ser Arg Pro Tyr His Lys Arg Met
146         435             440             445
148 gac cgc gtc ctg atg cac tat gta cgt gca gca gaa atg ctt tcc gcc        1392
149 Asp Arg Val Leu Met His Tyr Val Arg Ala Ala Glu Met Leu Ser Ala
150     450             455             460
152 tgg cac tcc tgg gac ggt atg gcc cgc atc gag gaa cgt ctg gag cag        1440
153 Trp His Ser Trp Asp Gly Met Ala Arg Ile Glu Glu Arg Leu Glu Gln
154 465             470             475             480
156 gcc cgc agg gag ctg tca ttg ttc cag cac cac gac ggt ata act ggc        1488
157 Ala Arg Arg Glu Leu Ser Leu Phe Gln His His Asp Gly Ile Thr Gly
158             485             490             495
160 aca gca aaa acg cac gta gtc gtc gac tac gag caa cgc atg cag gaa        1536
161 Thr Ala Lys Thr His Val Val Val Asp Tyr Glu Gln Arg Met Gln Glu
162     500             505             510
164 gct tta aaa gcc tgt caa atg gta atg caa cag tcg gtc tac cga ttg        1584
165 Ala Leu Lys Ala Cys Gln Met Val Met Gln Gln Ser Val Tyr Arg Leu
166         515             520             525
168 ctg aca aag ccc tcc atc tac agt ccg gac ttc agt ttc ycg tac ttt        1632
169 Leu Thr Lys Pro Ser Ile Tyr Ser Pro Asp Phe Ser Phe Xaa Tyr Phe
170     530             535             540
172 acg ctc gac gac tcc cgc tgg cca gga tct ggt gtg gag gac agt cga        1680
173 Thr Leu Asp Asp Ser Arg Trp Pro Gly Ser Gly Val Glu Asp Ser Arg
174 545             550             555             560
176 acc acc ata ata ctg ggc gag gat ata ctg ccc tcc aag cat gtg gtg        1728
177 Thr Thr Ile Ile Leu Gly Glu Asp Ile Leu Pro Ser Lys His Val Val
178             565             570             575
180 atg cac aac acc ctg ccc cac tgg cgg gag cag ctg gtg gac ttt tat        1776
181 Met His Asn Thr Leu Pro His Trp Arg Glu Gln Leu Val Asp Phe Tyr
182             580             585             590
184 gta tcc agt ccg ttt gta agc gtt acc gac ttg gca aac aat ccg gtg        1824
185 Val Ser Ser Pro Phe Val Ser Val Thr Asp Leu Ala Asn Asn Pro Val
186         595             600             605
188 gag gct cag gtg tcc ccg gtg tgg agc tgg cac cac gac aca ctc aca        1872
189 Glu Ala Gln Val Ser Pro Val Trp Ser Trp His His Asp Thr Leu Thr
190     610             615             620
192 aag act atc cac cca caa ggc tcc acc acc aag tac cgc atc atc ttc        1920
193 Lys Thr Ile His Pro Gln Gly Ser Thr Thr Lys Tyr Arg Ile Ile Phe
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/960,226

DATE: 01/28/2002
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Input Set : A:\12243-19SeqLst.txt
Output Set: N:\CRF3\01282002\I960226.raw

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194 625                    630                    635                    640
196 aag gct cgg gtg ccg ccc atg ggc ttg gcc acc tac gtt tta acc atc      1968
197 Lys Ala Arg Val Pro Pro Met Gly Leu Ala Thr Tyr Val Leu Thr Ile
198         645                    650                    655
200 tcc gat tcc aag cca gag cac acc tcg tat gca tcg aat ctc ttg ctc      2016
201 Ser Asp Ser Lys Pro Glu His Thr Ser Tyr Ala Ser Asn Leu Leu Leu
202         660                    665                    670
204 cgt aaa aac ccg act tcg tta cca ttg ggc caa tat ccg gag gat gtg      2064
205 Arg Lys Asn Pro Thr Ser Leu Pro Leu Gly Gln Tyr Pro Glu Asp Val
206         675                    680                    685
208 aag ttt ggc gat cct cga gag atc tca ttg cgg gtt ggt aac gga ccc      2112
209 Lys Phe Gly Asp Pro Arg Glu Ile Ser Leu Arg Val Gly Asn Gly Pro
210         690                    695                    700
212 acc ttg gcc ttt tcg gag cag ggt ctc ctt aag tcc att cag ctt act      2160
213 Thr Leu Ala Phe Ser Glu Gln Gly Leu Leu Lys Ser Ile Gln Leu Thr
214 705                    710                    715                    720
216 cag gat agc cca cat gta ccg gtg cac ttc aag ttc ctc aag tat ggc      2208
217 Gln Asp Ser Pro His Val Pro Val His Phe Lys Phe Leu Lys Tyr Gly
218         725                    730                    735
220 gtt cga tcg cat ggc gat aga tcc ggt gcc tat ctg ttc ctg ccc aat      2256
221 Val Arg Ser His Gly Asp Arg Ser Gly Ala Tyr Leu Phe Leu Pro Asn
222         740                    745                    750
224 gga cca gct tcg cca gtc gag ctt ggc cag cca gtg gtc ctg gtg act      2304
225 Gly Pro Ala Ser Pro Val Glu Leu Gly Gln Pro Val Val Leu Val Thr
226         755                    760                    765
228 aag ggc aaa ctg gag tcg tcc gtg agc gtg gga ctt ccg agc gtg gtg      2352
229 Lys Gly Lys Leu Glu Ser Ser Val Ser Val Gly Leu Pro Ser Val Val
230         770                    775                    780
232 cac cag acg ata atg cgc ggt ggt gca cct gag att cgc aat ctg gtg      2400
233 His Gln Thr Ile Met Arg Gly Gly Ala Pro Glu Ile Arg Asn Leu Val
234 785                    790                    795                    800
236 gat ata ggc tca ctg gac aac acg gag atc gtg atg cgc ttg gag acg      2448
237 Asp Ile Gly Ser Leu Asp Asn Thr Glu Ile Val Met Arg Leu Glu Thr
238         805                    810                    815
240 cat atc gac agc ggc gat atc ttc tac acg gat ctc aat gga ttg caa      2496
241 His Ile Asp Ser Gly Asp Ile Phe Tyr Thr Asp Leu Asn Gly Leu Gln
242         820                    825                    830
244 ttt atc aag agg cgg cgt ttg gac aaa tta cct ttg cag gcc aac tat      2544
245 Phe Ile Lys Arg Arg Arg Leu Asp Lys Leu Pro Leu Gln Ala Asn Tyr
246         835                    840                    845
248 tat ccc ata cct tcg ggt atg ttc att gag gat gcc aat acg cga ctc      2592
249 Tyr Pro Ile Pro Ser Gly Met Phe Ile Glu Asp Ala Asn Thr Arg Leu
250         850                    855                    860
252 act ctc ctc acg ggt caa ccg ctg ggt gga tct tct ctg gcc tcg ggc      2640
253 Thr Leu Leu Thr Gly Gln Pro Leu Gly Gly Ser Ser Leu Ala Ser Gly
254 865                    870                    875                    880
256 gag cta gag att atg caa gat cgt cgc ctg gcc agc gat gat gaa cgc      2688
257 Glu Leu Glu Ile Met Gln Asp Arg Arg Leu Ala Ser Asp Asp Glu Arg
258         885                    890                    895
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RAW SEQUENCE LISTING   DATE: 01/28/2002
PATENT APPLICATION: US/09/960,226   TIME: 13:49:07

Input Set : A:\12243-19SeqLst.txt
Output Set: N:\CRF3\01282002\I960226.raw

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260 ggc ctg gga cag ggt gtt ttg gac aac aag ccg gtg ctg cat att tat    2736
261 Gly Leu Gly Gln Gly Val Leu Asp Asn Lys Pro Val Leu His Ile Tyr
262             900                 905                 910
264 cgg ctg gtg ctg gag aag gtt aac aac tgt gtc cga ccg tca aag ctt    2784
265 Arg Leu Val Leu Glu Lys Val Asn Asn Cys Val Arg Pro Ser Lys Leu
266             915                 920                 925
268 cat cct gcc ggc tat ttg aca agt gcc gca cac aaa gca tcg cag tca    2832
269 His Pro Ala Gly Tyr Leu Thr Ser Ala Ala His Lys Ala Ser Gln Ser
270             930                 935                 940
272 ctg ctg gat cca ctg gac aag ttt ata ttc gct gaa aat gag tgg atc    2880
273 Leu Leu Asp Pro Leu Asp Lys Phe Ile Phe Ala Glu Asn Glu Trp Ile
274 945                 950                 955                 960
276 ggg gca cag ggg caa ttt ggt ggc gat cat cct tcg gct cgt gag gat    2928
277 Gly Ala Gln Gly Gln Phe Gly Gly Asp His Pro Ser Ala Arg Glu Asp
278             965                 970                 975
280 ctc gat gtg tcg gtg atg aga cgc tta acc aag agc tcg gcc aaa acc    2976
281 Leu Asp Val Ser Val Met Arg Arg Leu Thr Lys Ser Ser Ala Lys Thr
282             980                 985                 990
284 cag cga gta ggc tac gtt ctg cac  cgc acc aat ctg atg  caa tgc ggc   3024
285 Gln Arg Val Gly Tyr Val Leu His  Arg Thr Asn Leu Met  Gln Cys Gly
286             995                 1000                1005
288 act cca  gag gag cat aca cag  aag ctg gat gtg tgc  cac cta ctg       3069
289 Thr Pro  Glu Glu His Thr Gln  Lys Leu Asp Val Cys  His Leu Leu
290     1010                1015                1020
292 ccg aat  gtg gcg aga tgc gag  gcg acg acg ctg act  ttc ctg cag       3114
293 Pro Asn  Val Ala Arg Cys Glu  Ala Thr Thr Leu Thr  Phe Leu Gln
294     1025                1030                1035
296 aat ttg  gag cac ttg gat ggc  atg gtg gcg ccg gaa  gtg tgc ccc       3159
297 Asn Leu  Glu His Leu Asp Gly  Met Val Ala Pro Glu  Val Cys Pro
298     1040                1045                1050
300 atg gaa  acc gcc gct tat gtg  agc agt cac tca agc  tga                3198
301 Met Glu  Thr Ala Ala Tyr Val  Ser Ser His Ser Ser
302     1055                1060                1065
305 <210> SEQ ID NO: 2
306 <211> LENGTH: 1065
307 <212> TYPE: PRT
308 <213> ORGANISM: Drosophila melanogaster
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION: (542)..(542)
313 <223> OTHER INFORMATION: The 'Xaa' at location 542 stands for Pro, or Ser.
315 <400> SEQUENCE: 2
317 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala Phe Val Gly Leu Ser
318 1               5                   10                  15
321 Leu Gly Arg Ser Ser His His His His His His Gly Glu Phe Asp Asp
322             20                  25                  30
325 Pro Ile Arg Pro Pro Leu Lys Val Ala Arg Ser Pro Arg Pro Gly Gln
326             35                  40                  45
329 Cys Gln Asp Val Val Gln Asp Val Pro Asn Val Asp Val Gln Met Leu
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 01/28/2002
PATENT APPLICATION: US/09/960,226   TIME: 13:49:08

Input Set : A:\12243-19SeqLst.txt
Output Set: N:\CRF3\01282002\I960226.raw

L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9